

AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions and listings of claims in the application:

1. (Currently Amended) A method of analyzing a collection of genetically modified cell strains that are congenic with a parent strain wherein the genetically modified cell strains are yeast strains, the method comprising:
 - (a) receiving images of phenotypes for each of the genetically modified cell strains;
 - (b) analyzing the images with one or more algorithms that provide quantitative representations of the phenotypes; and
 - (c) comparing the quantitative representations of the phenotypes with a quantitative representation of a phenotype of a cell that is genetically similar or identical to one or more of the cell strains, and wherein the cell that is genetically similar or identical has been treated with a drug or a drug candidate.
2. (Original) The method of claim 1, wherein the genetically modified cell strains are deletion mutants having one or more genes deleted from the genome of the parent strain.
3. (Original) The method of claim 2, wherein the deletion mutants each lack a single gene present in the parent strain.
4. (Original) The method of claim 3, wherein the collection of genetically modified cell strains contains a deletion mutant for each non-essential gene in the parent strain.
5. (Original) The method of claim 4, wherein the collection of genetically modified cell strains includes the deletion mutants provided by the *Saccharomyces cerevisiae* Deletion Consortium.

6. (Original) The method of claim 5, wherein the collection of genetically modified cell strains further comprises mutant strains having modified, but not deleted, essential genes of *Saccharomyces cerevisiae*.

7. (Currently Amended) A method of analyzing a collection of genetically modified cell strains that are congenic with a parent strain wherein the genetically modified cell strains are yeast strains, the method comprising:

marking one or more cell features of the genetically modified cell strains so that said features can be highlighted in the images of the phenotypes;

imaging the genetically modified cell strains to produce the images of the phenotypes, wherein the cell features are highlighted in the images of the phenotypes;

receiving images of phenotypes for each of the genetically modified cell strains;

analyzing the images with one or more algorithms that provide quantitative representations of the phenotypes; and

comparing the quantitative representations of the phenotypes with (i) each other, (ii) a quantitative representation of a phenotype of the parent strain, or (iii) a quantitative representation of a phenotype of a cell that is genetically similar or identical to one or more of the cell strains,

wherein the genetically modified cell strains are yeast strains and wherein marking one or more cell features comprises staining the yeast strains with a first stain for the cell wall, a second stain for the genetic material, and a third stain for the cytoskeleton..

8. (Cancelled)

9. (Currently Amended) The method of claim 7 8, wherein the first stain is concanavalin A, the second stain is DAPI, and the third stain is rhodamine phalloidin.

10. (Original) The method of claim 1, wherein analyzing the images comprises:

receiving the intensity versus position data from one or markers on the genetically modified cell strains;
quantifying geometrical information about said markers; and
quantifying biological information about said genetically modified cell strains.

11. (Original) The method of claim 10, wherein the quantitative representations of the phenotypes include one or both of the geometrical information and the biological information.

12. (Original) The method of claim 1, wherein comparing the quantitative representations of the phenotypes comprises comparing the quantitative representations of the phenotypes with each other to cluster the phenotypes and identify common functional traits shared between multiple genetic modifications.

13. (Cancelled)

14. (Original) The method of claim 1, further comprising generating a database including records identifying the phenotypes and the quantitative representations of the phenotypes.

15. (Original) The method of claim 14, further comprising linking the database with another database containing non-morphological information about the collection of genetically modified cell strains or similar, unmodified parent strains.

16. (Currently Amended) A computer program product comprising a machine readable medium on which is provided program instructions for analyzing a collection of genetically modified cell strains that are congenic with a parent strain wherein the genetically modified cell strains are yeast strains, the instructions comprising:

(a) code for receiving images of phenotypes for each of the genetically modified cell strains;

(b) code for analyzing the images with one or more algorithms that provide quantitative representations of the phenotypes; and

(c) code for comparing the quantitative representations of the phenotypes with a quantitative representation of a phenotype of a cell that is genetically similar or identical to one or more of the cell strains, and wherein the cell that is genetically similar or identical has been treated with a drug or a drug candidate.

17. (Original) The computer program product of claim 16, wherein the genetically modified cell strains are deletion mutants having one or more genes deleted from the genome of the parent strain.

18. (Original) The computer program product of claim 17, wherein the deletion mutants each lack a single gene present in the parent strain.

19. (Original) The computer program product of claim 18, wherein the collection of genetically modified cell strains contains a deletion mutant for each non-essential gene in the parent strain.

20. (Original) The computer program product of claim 19, wherein the collection of genetically modified cell strains includes the deletion mutants provided by the *Saccharomyces cerevisiae* Deletion Consortium.

21. (Original) The computer program product of claim 20, wherein the collection of genetically modified cell strains further comprises mutant strains having modified, but not deleted, essential genes of *Saccharomyces cerevisiae*.

22. (Original) The computer program product of claim 16, further comprising:

code for imaging the genetically modified cell strains to produce the images of the phenotypes, wherein one or more cell features are highlighted by marking in the images of the phenotypes.

23. (Original) The computer program product of claim 22, wherein the genetically modified cell strains are yeast strains and wherein marking one or more cell features was accomplished by staining the yeast strains with a first stain for the cell wall, a second stain for the genetic material, and a third stain for the cytoskeleton.

24. (Original) The computer program product of claim 23, wherein the first stain is concanavalin A, the second stain is DAPI, and the third stain is rhodamine phalloidin.

25. (Original) The computer program product of claim 16, wherein the code for analyzing the images comprises:

code for receiving the intensity versus position data from one or markers on the genetically modified cell strains;

code for quantifying geometrical information about said markers; and

code for quantifying biological information about said genetically modified cell strains.

26. (Original) The computer program product of claim 25, wherein the quantitative representations of the phenotypes include one or both of the geometrical information and the biological information.

27. (Original) The computer program product of claim 16, wherein the code for comparing the quantitative representations of the phenotypes comprises code for comparing the quantitative representations of the phenotypes with each other to cluster the phenotypes and identify common functional traits shared between multiple genetic modifications.

28. (Cancelled)

29. (Original) The computer program product of claim 16, further code for comprising generating a database including records identifying the phenotypes and the quantitative representations of the phenotypes.

30. (Original) The computer program product of claim 29, further comprising code for linking the database with another database containing non-morphological information about the collection of genetically modified cell strains or similar, unmodified parent strains.

31. (Currently Amended) A computing device comprising a memory device configured to store at least temporarily program instructions for analyzing a collection of genetically modified cell strains that are congenic with a parent strain wherein the genetically modified cell strains are yeast strains, the instructions comprising:

(a) code for receiving images of phenotypes for each of the genetically modified cell strains;

(b) code for analyzing the images with one or more algorithms that provide quantitative representations of the phenotypes; and

(c) code for comparing the quantitative representations of the phenotypes with a quantitative representation of a phenotype of a cell that is genetically similar or identical to one or more of the cell strains, and wherein the cell that is genetically similar or identical has been treated with a drug or a drug candidate.

32. (Previously Presented) The method of claim 7, wherein the genetically modified cell strains are deletion mutants having one or more genes deleted from the genome of the parent strain.

33. (Previously Presented) The method of claim 32, wherein the deletion mutants each lack a single gene present in the parent strain.

34. (Previously Presented) The method of claim 33, wherein the collection of genetically modified cell strains contains a deletion mutant for each non-essential gene in the parent strain.

35. (Previously Presented) The method of claim 34, wherein the collection of genetically modified cell strains includes the deletion mutants provided by the *Saccharomyces cerevisiae* Deletion Consortium.

36. (Previously Presented) The method of claim 35, wherein the collection of genetically modified cell strains further comprises mutant strains having modified, but not deleted, essential genes of *Saccharomyces cerevisiae*.

37. (Previously Presented) The method of claim 7, wherein analyzing the images comprises:

receiving the intensity versus position data from one or markers on the genetically modified cell strains;
quantifying geometrical information about said markers; and
quantifying biological information about said genetically modified cell strains.

38. (Previously Presented) The method of claim 37, wherein the quantitative representations of the phenotypes include one or both of the geometrical information and the biological information.

39. (Previously Presented) The method of claim 7, wherein comparing the quantitative representations of the phenotypes comprises comparing the quantitative representations of the phenotypes with each other to cluster the phenotypes and identify common functional traits shared between multiple genetic modifications.

40. (Previously Presented) The method of claim 7, further comprising generating a database including records identifying the phenotypes and the quantitative representations of the phenotypes.

41. (Previously Presented) The method of claim 40, further comprising linking the database with another database containing non-morphological information about the collection of genetically modified cell strains or similar, unmodified parent strains.

42. (Previously Presented) A computer program product comprising a machine readable medium on which is provided program instructions for analyzing a collection of genetically modified cell strains that are congenic with a parent strain wherein the genetically modified cell strains are yeast strains; wherein one or more cell features of the genetically modified cell strains have been marked so that said features can be highlighted in the images of the phenotype; and wherein said one or more cell features comprises staining the yeast strains with a first stain for the cell wall, a second stain for the genetic material, and a third stain for the cytoskeleton, the instructions comprising:

(a) code for receiving images of phenotypes for each of the genetically modified cell strains wherein the cell features are highlighted in said images of the phenotypes;

(b) code for analyzing the images with one or more algorithms that provide quantitative representations of the phenotypes; and

(c) code for comparing the quantitative representations of the phenotypes with (i) each other, (ii) a quantitative representation of the parent strain, or (iii) a quantitative representation of a phenotype of a cell that is genetically similar or identical to one or more of the cell strains

43. (Previously Presented) The computer program product of claim 42, wherein the genetically modified cell strains are deletion mutants having one or more genes deleted from the genome of the parent strain.

44. (Previously Presented) The computer program product of claim 43, wherein the deletion mutants each lack a single gene present in the parent strain.

45. (Previously Presented) The computer program product of claim 44, wherein the collection of genetically modified cell strains contains a deletion mutant for each non-essential gene in the parent strain.

46. (Previously Presented) The computer program product of claim 45, wherein the collection of genetically modified cell strains includes the deletion mutants provided by the *Saccharomyces cerevisiae* Deletion Consortium.

47. (Previously Presented) The computer program product of claim 46, wherein the collection of genetically modified cell strains further comprises mutant strains having modified, but not deleted, essential genes of *Saccharomyces cerevisiae*.

48. (Previously Presented) The computer program product of claim 42, wherein the first stain is concanavalin A, the second stain is DAPI, and the third stain is rhodamine phalloidin.

49. (Previously Presented) The computer program product of claim 42, wherein the code for analyzing the images comprises:

code for receiving the intensity versus position data from one or markers on the genetically modified cell strains;

code for quantifying geometrical information about said markers; and

code for quantifying biological information about said genetically modified cell strains.

50. (Previously Presented) The computer program product of claim 49, wherein the quantitative representations of the phenotypes include one or both of the geometrical information and the biological information.

51. (Previously Presented) The computer program product of claim 42, wherein the code for comparing the quantitative representations of the phenotypes comprises code for comparing the quantitative representations of the phenotypes with

each other to cluster the phenotypes and identify common functional traits shared between multiple genetic modifications.

52. (Previously Presented) The computer program product of claim 42, further code for comprising generating a database including records identifying the phenotypes and the quantitative representations of the phenotypes.

53. (Previously Presented) The computer program product of claim 52, further comprising code for linking the database with another database containing non-morphological information about the collection of genetically modified cell strains or similar, unmodified parent strains.

54. (Previously Presented) The method of claim 1, further comprising:-
marking one or more cell features of the genetically modified cell strains so that said features can be highlighted in the images of the phenotypes; and
imaging the genetically modified cell strains to produce the images of the phenotypes, wherein the cell features are highlighted in the images of the phenotypes.

55. (Previously Presented) The method of claim 1, wherein the genetically modified cell strains are yeast strains and wherein marking one or more cell features comprises staining the yeast strains with a first stain for the cell wall, a second stain for the genetic material, and a third stain for the cytoskeleton.

56. (Previously Presented) The method of claim 55, wherein the first stain is concanavalin A, the second stain is DAPI, and the third stain is rhodamine phalloidin.